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<b>(21) International Application Number:</b> PCT/US96/14563 <b>(22) International Filing Date:</b> 11 September 1996 (11.09.96)  <b>(30) Priority Data:</b> 60/003,824 15 September 1995 (15.09.95) US 9603486.3 20 February 1996 (20.02.96) GB  <b>(71) Applicant (for all designated States except US):</b> MERCK & CO., INC. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065 (US).  <b>(72) Inventor; and</b> <b>(75) Inventor/Applicant (for US only):</b> SALOWE, Scott, P. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065 (US).  <b>(74) Common Representative:</b> MERCK & CO., INC.; 126 East Lincoln Avenue, Rahway, NJ 07065 (US).		<b>(81) Designated States:</b> CA, JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
<b>(54) Title:</b> A HIGH THROUGHPUT ASSAY USING FUSION PROTEINS  <b>(57) Abstract</b>  This application describes a high throughput assay for screening for compounds which are capable of binding to a fusion protein which consists of a target protein and an FK506-binding protein.		

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TITLE OF THE INVENTION

## A HIGH THROUGHPUT ASSAY USING FUSION PROTEINS

BACKGROUND OF THE INVENTION

5                   Src homology 2 (SH2) domains are a family of homologous protein domains that share the common property of recognizing phosphorylated tyrosine residues in specific peptide contexts. They have routinely been expressed in *E. coli* as fusion proteins with glutathione-S-transferase (GST). This usually provides high level expression and  
10 straightforward affinity purification on glutathione-Sepharose. Ligand binding is then assayed by incubating the GST/SH2 with a radiolabeled phosphopeptide, precipitating the complex with glutathione-Sepharose, washing the beads, and then counting the beads to determine bound radioactivity [Isakov et al., *J. Exp. Med.*, 181, 375-380 (1995); Piccione  
15 et al., *Biochemistry*, 32, 3197-3202 (1993); Huyer et al., *Biochemistry*, 34, 1040-1049 (1995)]. There are several disadvantages to this procedure, particularly when applied to high-throughput screening for agonists, antagonists, or inhibitors as new leads for drug development. First, the radiolabeling of the peptide is carried out either enzymatically  
20 with a kinase and [<sup>32</sup>P]ATP or chemically with [<sup>125</sup>I]Bolton-Hunter reagent. In both cases, the isotopes are short-lived and thus require frequent preparation of material. In the case of enzymatic phosphorylation, the appropriate kinase must also be available in sufficient quantity to generate enough material for screening purposes.  
25 Second, the protocol requires separation of bound complex from free phosphopeptide by washing of the glutathione-Sepharose beads. This is a nonequilibrium procedure that risks dissociation of the bound ligand, particularly when off-rates are fast. Thus, there is the possibility of misleading results. Finally, due to the number of manipulations and  
30 centrifugations involved, the protocol is very tedious to conduct manually and is not readily adaptable to robotic automation to increase throughput.

Two additional methods for measuring the interaction of proteins and ligands that have been applied to SH2 domains are biospecific interaction analysis using surface plasmon resonance and

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isothermal titration calorimetry (Felder et al., *Mol. Cell. Biol.*, 13, 1449-1455 (1993); Panayotou et al., *Mol. Cell. Biol.*, 13, 3567-3576 (1993); Payne et al., *Proc. Natl. Acad. Sci. U.S.A.*, 90, 4902-4906 (1993); Morelock et al., *J. Med. Chem.* 38, 1309-18 (1995); Ladbury et al., *Proc. Natl. Acad. Sci. U.S.A.*, 92, 3199-3203 (1995); Lemmon et al., *Biochemistry*, 33, 5070-5076 (1994)). These techniques do not require a particular fusion partner for the SH2 domain, but do require sophisticated instrumentation that is not amenable to high throughput screening.

## 10 SUMMARY OF THE INVENTION

The instant invention covers a method of screening for compounds capable of binding to a fusion protein which comprises combining a test compound, a tagged ligand, a fusion protein (target protein, peptide linker and FK506-binding protein), a radiolabeled ligand, and coated scintillation proximity assay (SPA) beads, and then measuring the scintillation counts attributable to the binding of the tagged ligand to the fusion protein in the presence of the test compound relative to a control assay in the absence of the test compound, so as to determine the effect the test compound has on the binding of the tagged ligand. This invention provides an immediate means of making use of SPA technology for the functional assay of ligand binding to a single or multiple signal transduction domain(s), for example a phosphopeptide binding to an SH2 domain. The present invention does not require specialized radiochemical synthesis and is readily adaptable to robotic automation for high capacity screening for agonists, antagonists, and/or inhibitors.

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### BRIEF DESCRIPTION OF THE FIGURES

Figure 1.

- A.) Binding of the streptavidin SPA bead, biotinylated ligand and the fusion protein (SH2:FKBP), which emits a detectable signal; and
- 5 B.) Binding of the test compound and the fusion protein (SH2:FKBP), which results in no signal detection .

### DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a method of screening for compounds which preferentially bind to a target protein.

An embodiment of this invention is a method of screening for compounds capable of binding to a fusion protein which comprises the steps of:

- 15 a) mixing a test compound, a tagged ligand, the fusion protein, a radiolabeled ligand and coated scintillation proximity assay (SPA) beads;
- b) incubating the mixture for between about 1 hour and about 24 hours;
- 20 c) measuring the SPA bead-bound counts attributable to the binding of the tagged ligand to the fusion protein in the presence of the test compound using scintillation counting; and
- 25 d) determining the binding of the tagged ligand to the fusion protein in the presence of the test compound relative to a control assay run in the absence of the test compound.

The term "fusion protein" refers to a "target protein" fused to an "FK506-binding protein" (FKBP), the two proteins being separated by a "peptide linker".

- 30 A "peptide linker" may consist of a sequence containing from about 1 to about 20 amino acids, which may or may not include the sequence for a protease cleavage site. An example of a peptide linker which is a protease cleavage site is represented by the amino acid sequence GLPRGS.

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The term "target protein" refers to any protein that has a defined ligand. Included within this definition of target protein are single and multiple signal transduction domains, such as, but not limited to, Src homology 1 (SH1), Src homology 2 (SH2), Src homology 3 (SH3), and pleckstrin homology (PH) domains [Hanks & Hunter, *FASEB J.*, 9, 576-596 (1995); Bolen, *Curr. Opin. Immunol.*, 7, 306-311 (1995); Kuriyan & Cowburn, *Curr. Opin. Struct. Biol.*, 3, 828-837 (1993); Cohen et al., *Cell*, 80, 237-248 (1995)]. The term "SH1 domain" refers to a family of homologous protein domains that bind ATP and catalyze tyrosine phosphorylation of peptide and protein substrates. The term "SH2 domain" refers to a family of homologous protein domains that share the common property of recognizing phosphorylated tyrosine residues in specific peptide contexts. The term "SH3 domain" refers to a family of homologous protein domains that share the common property of recognizing polyproline type II helices. The term "PH domain" refers to a family of homologous protein domains that mediate both protein-protein and protein-lipid interactions. Examples of SH2 domains which may be utilized in the method of the invention include, but are not limited to, the single and tandem SH2 domains present in the tyrosine kinases ZAP, SYK and LCK. The DNA sequences were obtained from GenBank, National Center for Biotechnology Information, National Library of Medicine, 8600 Rockville Pike, Bethesda, MD 20894. The Accession Numbers for the sequences are: human ZAP (L05148); human SYK (L28824) and human LCK (X13529).

The term "tagged ligand" refers to a biotinylated or epitope tagged ligand for the target protein.

The term "radiolabeled ligand" refers to a [ $^3\text{H}$ ]- or [ $^{125}\text{I}$ ]-labeled ligand which binds to the FKBP. An example of a radiolabeled ligand useful in the instant invention is [ $^3\text{H}$ ]-dihydroFK506.

The term "coated scintillation proximity assay beads" (SPA beads) refers to streptavidin-coated scintillation proximity assay beads when the tagged ligand is biotinylated, and to anti-epitope antibody bound to anti-antibody-coated or protein A-coated scintillation proximity assay beads when the tagged ligand is epitope-tagged.

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The term "control assay" refers to the assay when performed in the presence of the tagged ligand, the fusion protein, the radiolabeled ligand and the coated scintillation proximity assay beads, but in the absence of the test compound.

- 5           The term FK506-binding proteins may include, but are not limited to, the below listed FKBP and FKBP homologues, which include a citation to the references which disclose them. This list is not intended to limit the scope of the invention.

10   **Mammalian**

FKBP-12

Galat et al., *Eur. J. Biochem.*, 216:689-707 (1993).

FKBP-12.6

Wiederrecht, G. and F. Etzkorn  
*Perspectives in Drug Discovery and Design*, 2:57-84 (1994).

15

FKBP-13

Galat et al., *supra*; Wiederrecht and Etzkorn, *supra*.

FKBP-25

Galat et al., *supra*; Wiederrecht and Etzkorn, *supra*.

20   FKBP-38

Wiederrecht and Etzkorn, *supra*.

FKBP-51

Baughman et al., *Mol. Cell. Biol.*, 8, 4395-4402(1995).

FKBP-52

Galat et al., *supra*.

25   **Bacteria**

Legionella pneumophila

Galat et al., *supra*.

Legionella micadei

Galat et al., *supra*.

Chlamydia trachomatis

Galat et al., *supra*.

E. coli fkpa

Horne, S.M. and K.D. Young, *Arch. Microbiol.*, 163:357-365 (1995).

30

E. coli slyD

Roof et al., *J. Biol. Chem.* 269:2902-2910 (1994).

E. coli orf149

Trandinh et al., *FASEB J.* 6:3410-3420 (1992).

- 6 -

- Neisseria meningitidis      Hacker, J. and G. Fischer, *Mol. Micro.*,  
10:445-456 (1993).  
Streptomyces chrysomallus      Hacker and Fischer, *supra*.

5    **Fungal**

- yeast FKBP-12      Cardenas et al., *Perspectives in Drug  
Discovery and Design*, 2:103-126  
(1994).  
yeast FKBP-13      Cardenas et al., *supra*.  
10 yeast NPR1(FPR3)      Cardenas et al., *supra*.  
Neurospora      Galat et al., *supra*.

A variety of host cells may be used in this invention,  
which include, but are not limited to, bacteria, yeast, bluegreen algae,  
15 plant cells, insect cells and animal cells.

Expression vectors are defined herein as DNA sequences  
that are required for the transcription of cloned copies of genes and the  
translation of their mRNAs in an appropriate host. Such vectors can  
be used to express genes in a variety of host cells, such as, bacteria,  
20 yeast, bluegreen algae, plant cells, insect cells and animal cells.

Specifically designed vectors allow the shuttling of DNA  
between hosts such as bacteria-yeast or bacteria-animal cells. An  
appropriately constructed expression vector may contain: an origin of  
replication for autonomous replication in host cells, selectable markers, a  
25 limited number of useful restriction enzyme sites, a potential for high  
copy number, and active promoters. A promoter is defined as a DNA  
sequence that directs RNA polymerase to bind to DNA and initiate RNA  
synthesis. A strong promoter is one which causes mRNAs to be initiated  
at high frequency. Expression vectors may include, but are not limited  
30 to, cloning vectors, modified cloning vectors, specifically designed  
plasmids or viruses. Commercially available vectors suitable for FKBP  
fusion protein expression include, but are not limited to pBR322  
(Promega), pGEX (Amersham), pT7 (USB), pET (Novagen), pIBI (IBI),  
pProEX-1 (Gibco/BRL), pBluescript II (Stratagene), pTZ18R and



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pTZ19R (USB), pSE420 (Invitrogen), pVL1392 (Invitrogen), pBlueBac (Invitrogen), pBacPAK (Clontech), pHIL (Invitrogen), pYES2 (Invitrogen), pCDNA (Invitrogen), pREP (Invitrogen) or the like.

5 The expression vector may be introduced into host cells via any one of a number of techniques including but not limited to transformation, transfection, infection, protoplast fusion, and electroporation.

*E. coli* containing an expression plasmid with the target gene fused to FKBP are grown and appropriately induced. The cells are then  
10 pelleted and resuspended in a suitable buffer. Although FKBP-12 lacks sequences that specifically direct it to the periplasm, FKBP fusions are primarily located there and can be released by a standard freeze/thaw treatment of the cell pellet. Following centrifugation, the resulting supernatant contains >80% pure FKBP fusion, which if desired can be  
15 purified further by conventional methods. Alternatively, the assay is not dependent on pure protein and the initial periplasmic preparation may be used directly. A thrombin site located between FKBP and the target protein can be used as a means to cleave FKBP from the fusion; such cleaved material may be a suitable negative control for subsequent  
20 assays.

A fusion protein which contains a single or multiple SH2 domain(s) may be purified by preparing an affinity matrix consisting of biotinylated phosphopeptide coupled to avidin or streptavidin immobilized on a solid support. A freeze/thaw extract is prepared from  
25 the cells which express the fusion protein and is loaded onto the affinity matrix. The desired fusion protein is then specifically eluted with phenyl phosphate.

To assay the formation of a complex between a target protein and its ligand, the tagged ligand is mixed with the FKBP fusion  
30 protein in a suitable buffer in the presence of the radiolabeled ligand in the well of a white microplate. After a suitable incubation period to allow complex formation to occur, coated SPA beads are added to capture the tagged ligand and any bound fusion protein. The plate is sealed, incubated for a sufficient period to allow the capture to go to

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completion, then counted in a multiwell scintillation counter. Screening for agonists/antagonists/inhibitors is carried out by performing the initial incubation prior to the capture step with SPA beads in the presence of a test compound(s) to determine whether they have an effect upon the binding of the tagged ligand to the fusion protein. This principle is illustrated by Figure 1.

The present invention can be understood further by the following examples, which do not constitute a limitation of the invention.

10

### EXAMPLE 1

#### Process for Preparing the FKBP fusion cloning vector

General techniques for modifying and expressing genes in various host cells can be found in Ausubel, F.M., Brent, R., Kingston, R.E., Moore, D.D., Seidman, J.G., Smith, J.A. and Struhl, K. Current Protocols in Molecular Biology (John Wiley & Sons, New York, New York, 1989). Sequences for a 3'- altered FKBP fragment that contained a glycine codon (GGT) in place of the stop (TGA) codon followed by a sequence encoding a thrombin site (Leu-Val-Pro-Arg) and *Bam*HI restriction site (GAATTC) were amplified using the polymerase chain reaction (PCR). The PCR reaction contained the following primers: 5'-GATCGCCATGGGAGTGCAGGTGGAAACCATCTCCCCA-3' and 5'-TACGAATTCTGGCGTGGATCCACGCGGAACCAGACCTTCCAGTTTAG-3' and a plasmid containing human FKBP-12 as the template. The resulting 367 base pair amplification product was ligated into the vector pCRII (Invitrogen) and the ligation mixture transformed into competent *Escherichia coli* cells. Clones containing an insert were identified using PCR with flanking vector primers. Dideoxy DNA sequencing confirmed the nucleotide sequence of one positive isolate. The altered 338 base pair FKBP fragment was excised from the pCRII plasmid using *Nco*I and *Bam*HI and ligated into *Nco*I and *Bam*HI digested pET9d (Novagen) plasmid. Competent *E. coli* were transformed with the ligation mixture, and colonies containing the insert were identified using PCR with primers encoding for flanking vector sequences. The FKBP fusion cloning vector is called pET9dFKBPt.

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## EXAMPLE 2

### Process for Preparing the FK-ZAP fusion expression vector

5           A DNA fragment encoding for the tandem SH2 domains of ZAP-70 was prepared by PCR to contain a *Bam*HI site at the 5'-end such that the reading frame was conserved with that of FKBP in the fusion vector. At the 3'-end, the fragment also incorporated a stop codon followed by a *Bam*HI site. The PCR reaction contained Molt-4 cDNA  
10 (Clontech) and the following primers:  
5'-ATTAGGATCCATGCCAGATCCTGCAGCTCACCTGCCCT-3' and  
5'-ATATGGATCCTTACCAGAGGCGTTGCT-3'. The fragment was cloned into a suitable vector, sequenced, digested with *Bam*HI, and the insert containing the SH2 domains ligated to *Bam*HI treated  
15 pET9dFKBPt, and transformed into *E. coli*. Clones containing inserts in the correct orientation were identified by PCR or restriction enzyme analysis. Plasmid DNA was prepared and used to transform BL21(DE3) cells.

20

## EXAMPLE 3

### Process for Preparing the FK-SYK fusion expression vector

          The expression vector for the tandem SH2 domains of Syk fused to FKBP was prepared as in Example 2 except that the PCR  
25 reaction contained Raji cell cDNA (Clontech) and the following primers:  
5'-CAATAGGATCCATGGCCAGCAGCGGCATGGCTGA-3' and  
5'-GACCTAGGATCCCTAATTAAACATTTCCCTGTGTGCCGAT-3'.

30

## EXAMPLE 4

### Process for Preparing the FK-LCK fusion expression vector

          The expression vector for the SH2 domain of Lck fused to FKBP was prepared as in Example 2 except that the PCR reaction contained Molt-4 cDNA (Clontech) and the following primers:

- 10 -

5'-ATATGGATCCATGGCGAACAGCCTGGAGCCCGAACCCT-3'  
and  
5'-ATTAGGATCCTTAGGTCTGGCAGGGGCGGCTCAACCGTGT  
GCA-3'.

5

### EXAMPLE 5

#### FK-ZAP

- 10 Step A: Process for Expression of FK-ZAP  
*E. coli* BL21(DE3) cells containing the pET9dFKBPt/  
ZapSH2 plasmid were grown in Luria-Bertani (LB) media containing 50  
microgram/ml kanamycin at 37 degrees C until the optical density  
measured at 600 nm was 0.5-1.0. Expression of the FK-ZAP fusion  
15 protein was induced with 0.1 mM isopropyl beta-thiogalactopyranoside  
and the cells were grown for another 3-5 hr at 30 degrees C. They were  
pelleted at 4400 x g for 10 min at 4 degrees C and resuspended in 2% of  
the original culture volume with 100 mM tris pH 8.0 containing 1  
microgram/ml each aprotinin, pepstatin, leupeptin, and bestatin. The  
20 resuspended pellet was frozen at -20 degrees C until further purification.

#### Step B: Process for Purification of FK-ZAP

- The affinity matrix for purification of FK-ZAP was prepared  
by combining agarose-immobilized avidin with excess biotinylated  
25 phosphopeptide derived from the  $\zeta$ 1 ITAM sequence of the human T-cell  
receptor, biotinyl-GSNQLpYNELNLGRREEpYDVLDK, and washing  
out unbound peptide. Frozen cells containing FK-ZAP were thawed in  
warm water, refrozen on dry ice for about 25 min., then thawed again.  
After the addition of 0.1% octyl glucoside, 1 mM dithiothreitol (DTT)  
30 and 500 mM NaCl, the extract was centrifuged at 35,000 x g for  
approximately 30 minutes. The supernatant was loaded onto the  
phosphopeptide affinity column, at about 4° and washed with phosphate  
buffered saline containing 1 mM DTT and 0.1% octyl glucoside.  
FK-ZAP was eluted with 200 mM phenyl phosphate in the same buffer at  
35 about 37°. The protein pool was concentrated and the phenyl phosphate

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removed on a desalting column. The purified FK-ZAP was stored at about -30° in 10 mM HEPES/150 mM NaCl/1 mM DTT/0.1 mM EDTA/10% glycerol.

5

#### EXAMPLE 6

##### FK-SYK

*E. coli* BL21(DE3) cells containing the pET9dFKBPt/SykSH2 plasmid were grown, induced, and harvested as described in  
10 Example 5. FK-SYK was purified using the same affinity matrix and methodology described in Example 5.

#### EXAMPLE 7

15 FK-LCK

*E. coli* BL21(DE3) cells containing the pET9dFKBPt/LckSH2 plasmid were grown, induced, and harvested as described in Example 5. The affinity matrix for purification of FK-LCK was prepared  
20 by combining agarose-immobilized avidin with excess biotinyl-EPQpYEEIPIYL, and washing out unbound peptide. The remaining methodology for purification was the same as Example 5.

#### EXAMPLE 8

25

##### Method of Screening for Antagonists of FK-ZAP

Assays were conducted at ambient temperature in a buffer consisting of 25 mM HEPES, 10 mM DTT, 0.01% TWEEN-20, pH 7.0. 10 µl of a DMSO solution of test compound(s) and 120 µl of biotinyl-phosphopeptide stock solution were dispensed into the wells of a 96-well  
30 Packard Optiplate. Next, 20 µl of a mixture of FK-ZAP protein and <sup>3</sup>H-dihydroFK506 were added to each test well. Finally, 50 µl of a 4 mg/ml suspension of SPA beads were dispensed to each well. Final concentrations of the assay components were:

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25 nM biotinyl-GSNQLpYNELNLGRREEpYDVLDK  
25 nM FK-ZAP fusion protein  
10 nM <sup>3</sup>H-dihydroFK506 (DuPont NEN)  
1.0 mg/ml streptavidin-SPA beads (Amersham)  
5% DMSO

5

The plate was sealed and incubated between 1 and 8 hours. Bead-bound radioactivity was then measured in a Packard Topcount microplate scintillation counter.

10

#### EXAMPLE 9

##### Method of Screening for Antagonists of FK-SYK

The assays were conducted as set forth in Example 8, except that FK-SYK replaced FK-ZAP.

15

#### EXAMPLE 10

##### Method of Screening for Antagonists of FK-LCK

The assays were conducted as set forth in Example 8, except that FK-LCK replaced FK-ZAP and the tagged ligand was 25 nM biotinyl-EPQpYEEIPIYL.

20

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Salowe, Scott P.
- (ii) TITLE OF INVENTION: A High Throughput Assay Using Fusion Proteins
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
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  - (C) CITY: Rahway
  - (D) STATE: NJ
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 07065
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Camara, Valerie J.
  - (B) REGISTRATION NUMBER: 35,090
  - (C) REFERENCE/DOCKET NUMBER: 19494
- (ix) TELECOMMUNICATION INFORMATION:
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  - (B) TELEFAX: (908) 594-4720

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1137 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

- 14 -

ATGGGAGTGC AGGTGGAAAC CATCTCCCCA GGAGATGGAC GCACCTTCCC CAAGCGCGGC	60
CAGACCTGCG TGGTGCACTA CACCGGGATG CTTGAAGATG GAAAGAAATT TGATTCTCTC	120
CGGGACAGAA ACAAGCCCTT TAAGTTTATG CTAGGCAAGC AGGAGGTGAT CCGAGGCTGG	180
GAAGAAGGGG TTGCCCAGAT GAGTGTGGGT CAGAGAGCCA AACTGACTAT ATCTCCAGAT	240
TATGCCTATG GTGCCACTGG GCACCCAGGC ATCATCCAC CACATGCCAC TCTCGTCTTC	300
GATGTGGAGC TTCTAAAACT GGAAGGTCTG GTTCCGCGTG GATCCATGCC AGATCCTGCA	360
GCTCACCTGC CCTTCTTCTA CGGCAGCATC TCGCGTGCCG AGGCCGAGGA GCACCTGAAG	420
CTGGCGGGCA TGGCGGACGG GCTCTTCCTG CTGCGCCAGT GCCTGCGCTC GCTGGGCGGC	480
TATGTGCTGT CGCTCGTGCA CGATGTGCGC TTCCACCACT TTCCCATCGA GCGCCAGCTC	540
AACGGCACCT ACGCCATTGC CGGCGGCAAA GCGCACTGTG GACCGGCAGA GCTCTGCGAG	600
TTCTACTCGC GCGACCCCGA CGGGCTGCCC TGCAACCTGC GCAAGCCGTG CAACCGGCCG	660
TGGGGCTCG AGCCGAGCC GGGGTCTTC GACTGCCTGC GAGACGCCAT GGTGCGTGAC	720
TACGTGCGCC AGACCTGGAA GCTGGAGGGC GAGGCCCTGG AGCAGGCCAT CATCAGCCAG	780
GCCCCGAGG TGGAGAAGCT CATTGCTACG ACGGCCACG AGCGGATGCC CTGGTACCAC	840
AGCAGCCTGA CGCGTGAGGA GGCCGAGCGT AAACCTTTACT CTGGGGCGCA GACCGACGGC	900
AAGTTCTGTC TGAGGCCGCG GAAGGAGCAG GGCACATACG CCCTGTCCCT CATCTATGGG	960
AAGACGGTGT ACCACTACCT CATCAGCCAA GACAAGGCGG GCAAGTACTG CATTCCCGAG	1020
GGCACCAAGT TTGACACGCT CTGGCAGCTG GTGGAGTATC TGAAGCTGAA GCGGACGGG	1080
CTCATCTACT GCCTGAAGGA GGCCTGCCCC AACAGCAGTG CCAGCAACGC CTCTTAA	1137

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGGAGTGC AGGTGGAAAC CATCTCCCCA GGAGATGGAC GCACCTTCCC CAAGCGCGGC	60
CAGACCTGCG TGGTGCACTA CACCGGGATG CTTGAAGATG GAAAGAAATT TGATTCTCTC	120



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CGGGACAGAA ACAAGCCCTT TAAGTTTATG CTAGGCAAGC AGGAGGTGAT CCGAGGCTGG	180
GAAGAAGGGG TTGCCCAGAT GAGTGTGGGT CAGAGAGCCA AACTGACTAT ATCTCCAGAT	240
TATGCCTATG GTGCCACTGG GCACCCAGGC ATCATCCCAC CACATGCCAC TCTCGTCTTC	300
GATGTGGAGC TTCTAAAACT GGAAGGTCTG GTTCCGCGTG GATCCATGGC CAGCAGCGGC	360
ATGGCTGACA GCGCCAACCA CCTGCCCTTC TTTTTCGGCA ACATCACCCG GGAGGAGGCA	420
GAAGATTACC TGGTCCAGGG GGGCATGAGT GATGGGCTTT ATTTGCTGCG CCAGAGCCGC	480
AACTACCTGG GTGGCTTCGC CCTGTCCGTG GCCCACGGGA GGAAGGCACA CCACTACACC	540
ATCGAGCGGG AGCTGAATGG CACCTACGCC ATCGCCGGTG GCAGGACCCA TGCCAGCCCC	600
GCCGACCTCT GCCACTACCA CTCCCAGGAG TCTGATGGCC TGGTCTGCCT CCTCAAGAAG	660
CCCTTCAACC GGCCCCAAGG GGTGCAGCCC AAGACTGGGC CCTTTGAGGA TTTGAAGGAA	720
AACCTCATCA GGGAAATATGT GAAGCAGACA TGGAACTGC AGGGTCAGGC TCTGGAGCAG	780
GCCATCATCA GTCAGAAGCC TCAGCTGGAG AAGCTGATCG CTACCACAGC CCATGAAAAA	840
ATGCCTTGGT TCCATGGAAA AATCTCTCGG GAAGAATCTG AGCAAATTGT CCTGATAGGA	900
TCAAAGACAA ATGGAAAGTT CCTGATCCGA GCCAGAGACA ACAACGGCTC CTACGCCCTG	960
TGCCTGCTGC ACGAAGGGAA GGTGCTGCAC TATCGCATCG ACAAAGACAA GACAGGGAAG	1020
CTCTCCATCC CCGAGGGAAA GAAGTTCGAC ACGCTCTGGC AGCTAGTCGA GCATTATTCT	1080
TATAAAGCAG ATGTTTGTGTT AAGAGTTCTT ACTGTCCCAT GTCAAAAAT CGGCACACAG	1140
GGAAATGTTA ATTAG	1155

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGGAGTGC AGGTGGAAAC CATCTCCCCA GGAGATGGAC GCACCTTCCC CAAGCGCGGC	60
CAGACCTGCG TGGTGCACTA CACCGGGATG CTTGAAGATG GAAAGAAATT TGATTCTCTC	120

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CGGGACAGAA ACAAGCCCTT TAAGTTTATG CTAGGCAAGC AGGAGGTGAT CCGAGGCTGG      180
GAAGAAGGGG TTGCCCAGAT GAGTGTGGGT CAGAGAGCCA AACTGACTAT ATCTCCAGAT      240
TATGCCTATG GTGCCACTGG GCACCCAGGC ATCATCCCAC CACATGCCAC TCTCGTCTTC      300
GATGTGGAGC TTCTAAAACT GGAAGGTCTG GTTCCGCGTG GATCCATGGC GAACAGCCTG      360
GAGCCCGAAC CCTGGTTCTT CAAGAACCTG AGCCGCAAGG ACGCGGAGCG GCAGCTCCTG      420
GCGCCCGGGA ACACTCACGG CTCCTTCCTC ATCCGGGAGA GCGAGAGCAC CGCGGGATCG      480
TTTTCACTGT CGGTCCGGGA CTTCGACCAG AACCAGGGAG AGGTGGTGAA ACATTACAAG      540
ATCCGTAATC TGGACAACGG TGGCTTCTAC ATCTCCCCTC GAATCACTTT TCCCGGCCTG      600
CATGAACTGG TCCGCCATTA CACCAATGCT TCAGATGGGC TGTGCACACG GTTGAGCCGC      660
CCCTGCCAGA CCTAA                                                                675

```

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
 1           5           10           15
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
 20           25           30
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35           40           45
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50           55           60
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65           70           75           80
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85           90           95
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Leu Val Pro
100           105           110

```

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Arg	Gly	Ser	Met	Pro	Asp	Pro	Ala	Ala	His	Leu	Pro	Phe	Phe	Tyr	Gly	115	120	125
Ser	Ile	Ser	Arg	Ala	Glu	Ala	Glu	Glu	His	Leu	Lys	Leu	Ala	Gly	Met	130	135	140
Ala	Asp	Gly	Leu	Phe	Leu	Leu	Arg	Gln	Cys	Leu	Arg	Ser	Leu	Gly	Gly	145	150	155
Tyr	Val	Leu	Ser	Leu	Val	His	Asp	Val	Arg	Phe	His	His	Phe	Pro	Ile	165	170	175
Glu	Arg	Gln	Leu	Asn	Gly	Thr	Tyr	Ala	Ile	Ala	Gly	Gly	Lys	Ala	His	180	185	190
Cys	Gly	Pro	Ala	Glu	Leu	Cys	Glu	Phe	Tyr	Ser	Arg	Asp	Pro	Asp	Gly	195	200	205
Leu	Pro	Cys	Asn	Leu	Arg	Lys	Pro	Cys	Asn	Arg	Pro	Ser	Gly	Leu	Glu	210	215	220
Pro	Gln	Pro	Gly	Val	Phe	Asp	Cys	Leu	Arg	Asp	Ala	Met	Val	Arg	Asp	225	230	235
Tyr	Val	Arg	Gln	Thr	Trp	Lys	Leu	Glu	Gly	Glu	Ala	Leu	Glu	Gln	Ala	245	250	255
Ile	Ile	Ser	Gln	Ala	Pro	Gln	Val	Glu	Lys	Leu	Ile	Ala	Thr	Thr	Ala	260	265	270
His	Glu	Arg	Met	Pro	Trp	Tyr	His	Ser	Ser	Leu	Thr	Arg	Glu	Glu	Ala	275	280	285
Glu	Arg	Lys	Leu	Tyr	Ser	Gly	Ala	Gln	Thr	Asp	Gly	Lys	Phe	Leu	Leu	290	295	300
Arg	Pro	Arg	Lys	Glu	Gln	Gly	Thr	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Gly	305	310	315
Lys	Thr	Val	Tyr	His	Tyr	Leu	Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	325	330	335
Cys	Ile	Pro	Glu	Gly	Thr	Lys	Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	340	345	350
Tyr	Leu	Lys	Leu	Lys	Ala	Asp	Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	355	360	365
Cys	Pro	Asn	Ser	Ser	Ala	Ser	Asn	Ala	Ser							370	375	

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid

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(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1           5           10           15
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20           25           30
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35           40           45
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50           55           60
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65           70           75           80
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85           90           95
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Leu Val Pro
100          105          110
Arg Gly Ser Met Ala Ser Ser Gly Met Ala Asp Ser Ala Asn His Leu
115          120          125
Pro Phe Phe Phe Gly Asn Ile Thr Arg Glu Glu Ala Glu Asp Tyr Leu
130          135          140
Val Gln Gly Gly Met Ser Asp Gly Leu Tyr Leu Leu Arg Gln Ser Arg
145          150          155          160
Asn Tyr Leu Gly Gly Phe Ala Leu Ser Val Ala His Gly Arg Lys Ala
165          170          175
His His Tyr Thr Ile Glu Arg Glu Leu Asn Gly Thr Tyr Ala Ile Ala
180          185          190
Gly Gly Arg Thr His Ala Ser Pro Ala Asp Leu Cys His Tyr His Ser
195          200          205
Gln Glu Ser Asp Gly Leu Val Cys Leu Leu Lys Lys Pro Phe Asn Arg
210          215          220
Pro Gln Gly Val Gln Pro Lys Thr Gly Pro Phe Glu Asp Leu Lys Glu
225          230          235          240

```

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Asn Leu Ile Arg Glu Tyr Val Lys Gln Thr Trp Asn Leu Gln Gly Gln
      245                      250                      255

Ala Leu Glu Gln Ala Ile Ile Ser Gln Lys Pro Gln Leu Glu Lys Leu
      260                      265                      270

Ile Ala Thr Thr Ala His Glu Lys Met Pro Trp Phe His Gly Lys Ile
      275                      280                      285

Ser Arg Glu Glu Ser Glu Gln Ile Val Leu Ile Gly Ser Lys Thr Asn
      290                      295                      300

Gly Lys Phe Leu Ile Arg Ala Arg Asp Asn Asn Gly Ser Tyr Ala Leu
      305                      310                      315                      320

Cys Leu Leu His Glu Gly Lys Val Leu His Tyr Arg Ile Asp Lys Asp
      325                      330                      335

Lys Thr Gly Lys Leu Ser Ile Pro Glu Gly Lys Lys Phe Asp Thr Leu
      340                      345                      350

Trp Gln Leu Val Glu His Tyr Ser Tyr Lys Ala Asp Gly Leu Leu Arg
      355                      360                      365

Val Leu Thr Val Pro Cys Gln Lys Ile Gly Thr Gln Gly Asn Val Asn
      370                      375                      380

```

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1           5           10           15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
      20           25           30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
      35           40           45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
      50           55           60

```

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Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp  
 65 70 75 80  
 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala  
 85 90 95  
 Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Leu Val Pro  
 100 105 110  
 Arg Gly Ser Met Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe Phe Lys  
 115 120 125  
 Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn  
 130 135 140  
 Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala Gly Ser  
 145 150 155 160  
 Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu Val Val  
 165 170 175  
 Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr Ile Ser  
 180 185 190  
 Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His Tyr Thr  
 195 200 205  
 Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys Gln Thr  
 210 215 220

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WHAT IS CLAIMED IS:

1. A method of screening for compounds capable of binding to a fusion protein which comprises the steps of:
  - 5 a) mixing a test compound, a tagged ligand, the fusion protein, a radiolabeled ligand and coated scintillation proximity assay (SPA) beads;
  - b) incubating the mixture from between about 1 hour to about 24 hours;
  - 10 c) measuring the SPA bead-bound counts attributable to the binding of the tagged ligand to the fusion protein in the presence of the test compound using scintillation counting; and
  - 15 d) determining the binding of the tagged ligand to the fusion protein in the presence of the test compound relative to a control assay run in the absence of the test compound.
2. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 1, wherein the tagged  
20 ligand is a biotinylated ligand or epitope-tagged ligand.
3. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 2, wherein scintillation proximity assay beads are streptavidin-coated or anti-antibody or protein  
25 A-coated.
4. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 3, wherein the radiolabeled ligand consists of [<sup>3</sup>H]- or [<sup>125</sup>I]-labeled FK506 analog.  
30
5. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 4, wherein the fusion protein comprises an FK506-binding protein linked through a peptide linker to a target protein.

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6. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 5, wherein the target protein comprises a single or multiple signal transduction domain.

7. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 6, wherein the single or multiple signal transduction domain is selected from the group consisting of: SH1, SH2, SH3 and PH domains.

8. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 7, wherein the target protein is a single or multiple SH2 domain.

9. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 8, wherein the radiolabeled ligand is [<sup>3</sup>H]-dihydroFK506.

10. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 9, wherein the FK506-binding protein is a 12kDA human FK506-binding protein.

11. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 10, wherein the target protein is a single or multiple SH2 domain selected from the group consisting of: ZAP:SH2, SYK:SH2 and LCK:SH2.

12. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 11, wherein the target protein is the SH2 domain, ZAP:SH2.

13. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 11, wherein the target protein is the SH2 domain, SYK:SH2.

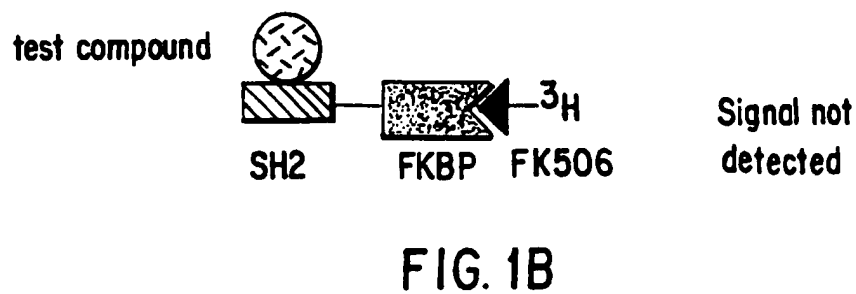
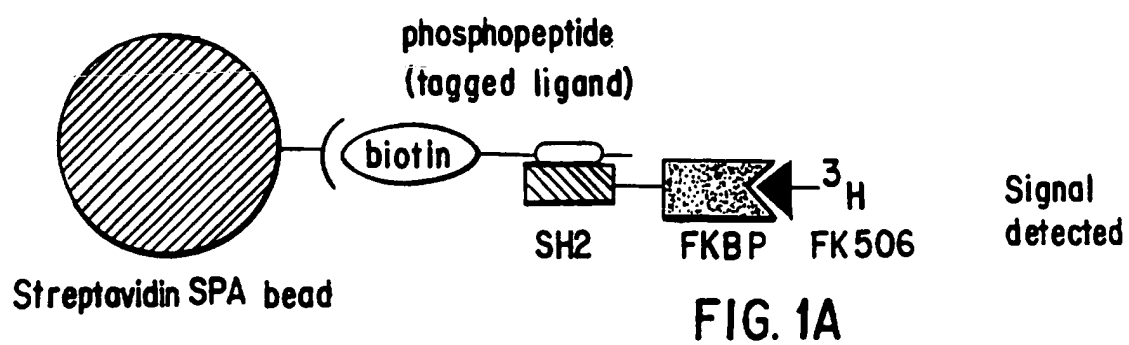


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14. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 11, wherein the target protein is the SH2 domain, LCK:SH2.

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# INTERNATIONAL SEARCH REPORT

Int. l. application No.  
PCT/US96/14563

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : G01N 33/53, 33/534

US CL : 435/7.5; 436/529

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.5; 436/529

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, EMBASE, BIOSIS, CAPLUS

search terms: scintillation proximity assay#, spa, fusion protein#, sh2 domain#, transduction domain#, target protein#, biotin?

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Sonatore et al. The Utility of FK506-Binding Protein as a Fusion Partner in Scintillation Proximity Assays: Application to SH2 Domains. Anal. Biochem. 1996, Vol. 240, pages 289-297.	1-14

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*E* earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means		
*P* document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

08 DECEMBER 1996

Date of mailing of the international search report

10 JAN 1997

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# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US96/14563

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Lerner et al. Scintillation Proximity Assay for Human DNA Topoisomerase I using Recombinant Biotiny Fusion Protein Produced in Baculovirus-Infected Insect Cells. Anal. Biochem. 1996, Vol. 240, pages 289-297.	
Y	Skinner et al. Direct Measurement of the Binding of RAS to Neurobromin using a Scintillation Proximity Assay. Anal. Biochem. 1994, Vol. 223, pages 259-265.	1,3